FIGURE 1

```
   1  AGAAAGGGGT GCGGCAGCAC TGCCAGGGGA AGAGGGTGAT CCGACCCGGG
  51  GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA GCGGCAGCCC CCGCCGCCCC
 101  CGCAGCCCCT TCTCCTCCTT TCTCCCACGT CCTATCTGCC TCTCGCTGGA
 151  GGCCAGGCCG TGCAGCATCG AAGACAGGAG GAACTGGAGC CTCATTGGCC
 201  GGCCCGGGGC GCCGGCCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG
 251  GGACCCGACC GCTGCCGGCC GCGCTCCCGC TGCTCCTGCC GGGTGATGGA
 301  AAACCCCAGC CCGGCCGCCG CCCTGGGCAA GGCCCTCTGC GCTCTCCTCC
 351  TGGCCACTCT CGGCGCCGCC GGCCAGCCTC TTGGGGGAGA GTCCATCTGT
 401  TCCGCCGGAG CCCCGGCCAA ATACAGCATC ACCTTCACGG GCAAGTGGAG
 451  CCAGACGGCC TTCCCCAAGC AGTACCCCCT GTTCCGCCCC CCTGCGCAGT
 501  GGTCTTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG
 551  AAGAACCAGT ACGTCAGTAA CGGGCTGCGC GACTTTGCGG AGCGCGGCGA
 601  GGCCTGGGCG CTGATGAAGG AGATCGAGGC GGCGGGGGAG GCGCTGCAGA
 651  GCGTGCACGC GGTGTTTTCG GCGCCCGCCG TCCCCAGCGG CACCGGGCAG
 701  ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG TCTCGTTTGT
 751  GGTGCGCATC GTGCCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG
 801  ACCTGTGCGA CGGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC
 851  CCCTACGACG CCGGGACGGA CAGCGGCTTC ACCTTCTCCT CCCCCAACTT
 901  CGCCACCATC CCGCAGGACA CGGTGACCGA GATAACGTCC TCCTCTCCCA
 951  GCCACCCGGC CAACTCCTTC TACTACCCAC GGCTGAAGGC CCTGCCTCCC
1001  ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA GGGCCTTCAT
1051  CCCTCCCGCC CCAGTCCTGC CCAGCAGGGA CAATGAGATT GTAGACAGCG
1101  CCTCAGTTCC AGAAACGCCG CTGGACTGCG AGGTCTCCCT GTGGTCGTCC
1151  TGGGGACTGT GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC
1201  TCGCTACGTC CGGGTCCAGC CCGCCAACAA CGGGAGCCCC TGCCCCGAGC
1251  TCGAAGAAGA GGCTGAGTGC GTCCCTGATA ACTGCGTCTA AGACCAGAGC
```

FIGURE 1 - continued

```
1301   CCCGCAGCCC CTGGGGCCCC CCGGAGCCAT GGGGTGTCGG GGGCTCCTGT

1351   GCAGGCTCAT GCTGCAGGCG GCCGAGGGCA CAGGGGGTTT CGCGCTGCTC

1401   CTGACCGCGG TGAGGCCGCG CCGACCATCT CTGCACTGAA GGGCCCTCTG

1451   GTGGCCGGCA CGGGCATTGG GAAACAGCCT CCTCCTTTCC CAACCTTGCT

1501   TCTTAGGGGC CCCCGTGTCC CGTCTGCTCT CAGCCTCCTC CTCCTGCAGG

1551   ATAAAGTCAT CCCCAAGGCT CCAGCTACTC TAAATTATGT CTCCTTATAA

1601   GTTATTGCTG CTCCAGGAGA TTGTCCTTCA TCGTCCAGGG GCCTGGCTCC

1651   CACGTGGTTG CAGATACCTC AGACCTGGTG CTCTAGGCTG TGCTGAGCCC

1701   ACTCTCCCGA GGGCGCATCC AAGCGGGGGC CACTTGAGAA GTGAATAAAT

1751   GGGGCGGTTT CGGAAGCGTC
```

FIGURE 2

```
  1   MENPSPAAAL GKALCALLLA TLGAAGQPLG GESICSAGAP AKYSITFTGK

 51   WSQTAFPKQY PLFRPPAQWS SLLGAAHSSD YSMWRKNQYV SNGLRDFAER

101   GEAWALMKEI EAAGEALQSV HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS

151   FVVRIVPSPD WFVGVDSLDL CDGDRWREQA ALDLYPYDAG TDSGFTFSSP

201   NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT LVRLRQSPRA

251   FIPPAPVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTKS

301   RTRYVRVQPA NNGSPCPELE EEAECVPDNC V
```

FIGURE 3

```
RG1      1 MENPSPAAALGKALCALLLATLGA.AGQPLGGESICSAGAPAKYSITFTG 49
           ||| |    .| : |    ||| ||. ||||||||||:|.|   |:||||||||
mindin 1 MENVS..FSLDRTLWVFLLAMLGSTAGQPLGGESVCTARPLARYSITFTG 48

        50 KWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAE 99
           |||||||||||||||||||||||||||||||||||||:||||||||||||
        49 KWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNEYVSNGLRDFAE 98

       100 RGEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLV 149
           ||||||||||||||| |||||||||||||||||||||||||   |||||
        99 RGEAWALMKEIEAAGEKLQSVHAVFSAPAVPSGTGQTSAELEVHPRHSLV 148

       150 SFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSS 199
           ||||||||||||||:||||||:|  ||:||  |||||:|||||||||||
       149 SFVVRIVPSPDWFVGIDSLDLCEGGRWKEQVVLDLYPHDAGTDSGFTFSS 198

       200 PNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPR 249
           |||||||||||||||.||||||||||||||.|||||:||  |||||||||
       199 PNFATIPQDTVTEITASSPSHPANSFYYPRLKSLPPIAKVTFVRLRQSPR 248

       250 AFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTK 299
           || ||.  | || |||||| ||||||||||||||||||||||| ||:|| |
       249 AFAPPSLDLASRGNEIVDSLSVPETPLDCEVSLWSSWGLCGGPCGKLGAK 298

       300 SRTRYVRVQPANNGSPCPELEEEAECVPDNCV 331
           |||||||||||||.||||||||||| |||||
       299 SRTRYVRVQPANNGTPCPELEEEAECAPDNCV 330
```

FIGURE 4

```
      AGAAAGGGGTGCGGCAGCACTGCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCT
   1  ---------+---------+---------+---------+---------+---------+  60
      TCTTTCCCCACGCCGTCGTGACGGTCCCCTTCTCCCACTAGGCTGGGCCCCTTCCAGCGA

      GGGCAGGGCGAGTTGGGAAAGCGGCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTT
  61  ---------+---------+---------+---------+---------+---------+  120
      CCCGTCCCGCTCAACCCTTTCGCCGTCGGGGGCGGCGGGGGCGTCGGGGAAGAGGAGGAA

      TCTCCCACGTCCTATCTGCCTCTCGCTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAG
 121  ---------+---------+---------+---------+---------+---------+  180
      AGAGGGTGCAGGATAGACGGAGAGCGACCTCCGGTCCGGCACGTCGTAGCTTCTGTCCTC

      GAACTGGAGCCTCATTGGCCGGCCCGGGGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGG
 181  ---------+---------+---------+---------+---------+---------+  240
      CTTGACCTCGGAGTAACCGGCCGGGCCCCGCGGCCGGAGCCCGAATTTATCCTCGAGGCC

      GCTCTGGCTGGGACCCGACCGCTGCCGGCCGCGCTCCCGCTGCTCCTGCCGGGTGATGGA
 241  ---------+---------+---------+---------+---------+---------+  300
      CGAGACCGACCCTGGGCTGGCGACGGCCGGCGCGAGGGCGACGAGGACGGCCCACTACCT

 b                                                          M  E  -

      AAACCCCAGCCCGGCCGCCGCCCTGGGCAAGGCCCTCTGCGCTCTCCTCCTGGCCACTCT
 301  ---------+---------+---------+---------+---------+---------+  360
      TTTGGGGTCGGGCCGGCGGCGGGACCCGTTCCGGGAGACGCGAGAGGAGGACCGGTGAGA

 b     N  P  S  P  A  A  A  L  G  K  A  L  C  A  L  L  L  A  T  L  -

      CGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTCCATCTGTTCCGCCGGAGCCCCGGCCAA
 361  ---------+---------+---------+---------+---------+---------+  420
      GCCGCGGCGGCCGGTCGGAGAACCCCCTCTCAGGTAGACAAGGCGGCCTCGGGGCCGGTT

 b     G  A  A  G  Q  P  L  G  G  E  S  I  C  S  A  G  A  P  A  K  -

      ATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCCAAGCAGTACCCCCT
 421  ---------+---------+---------+---------+---------+---------+  480
      TATGTCGTAGTGGAAGTGCCCGTTCACCTCGGTCTGCCGGAAGGGGTTCGTCATGGGGGA

 b     Y  S  I  T  F  T  G  K  W  S  Q  T  A  F  P  K  Q  Y  P  L  -

      GTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGGGCCGCGCATAGCTCCGACTACAG
 481  ---------+---------+---------+---------+---------+---------+  540
      CAAGGCGGGGGGACGCGTCACCAGAAGCGACGACCCCCGGCGCGTATCGAGGCTGATGTC

 b     F  R  P  P  A  Q  W  S  S  L  L  G  A  A  H  S  S  D  Y  S  -

      CATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCGCGACTTTGCGGAGCGCGGCGA
 541  ---------+---------+---------+---------+---------+---------+  600
      GTACACCTCCTTCTTGGTCATGCAGTCATTGCCCGACGCGCTGAAACGCCTCGCGCCGCT

 b     M  W  R  K  N  Q  Y  V  S  N  G  L  R  D  F  A  E  R  G  E  -
```

FIGURE 4 - continued

```
      GGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGGCGCTGCAGAGCGTGCACGC
  601 ---------+---------+---------+---------+---------+---------+ 660
      CCGGACCCGCGACTACTTCCTCTAGCTCCGCCGCCCCCTCCGCGACGTCTCGCACGTGCG

  b     A  W  A  L  M  K  E  I  E  A  A  G  E  A  L  Q  S  V  H  A  -

      GGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACGTCGGCGGAGCTGGAGGT
  661 ---------+---------+---------+---------+---------+---------+ 720
      CCACAAAAGCCGCGGGCGGCAGGGGTCGCCGTGGCCCGTCTGCAGCCGCCTCGACCTCCA

  b     V  F  S  A  P  A  V  P  S  G  T  G  Q  T  S  A  E  L  E  V  -

      GCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCCCAGCCCCGACTGGTT
  721 ---------+---------+---------+---------+---------+---------+ 780
      CGTCGCGTCCGTGAGCGACCAGAGCAAACACCACGCGTAGCACGGGTCGGGGCTGACCAA

  b     Q  R  R  H  S  L  V  S  F  V  V  R  I  V  P  S  P  D  W  F  -

      CGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGGAACAGGCGGCGCT
  781 ---------+---------+---------+---------+---------+---------+ 840
      GCACCCGCACCTGTCGGACCTGGACACGCTGCCCCTGGCAACCGCCCTTGTCCGCCGCGA

  b     V  G  V  D  S  L  D  L  C  D  G  D  R  W  R  E  Q  A  A  L  -

      GGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCCTCCCCCAACTT
  841 ---------+---------+---------+---------+---------+---------+ 900
      CCTGGACATGGGGATGCTGCGGCCCTGCCTGTCGCCGAAGTGGAAGAGGAGGGGGTTGAA

  b     D  L  Y  P  Y  D  A  G  T  D  S  G  F  T  F  S  S  P  N  F  -

      CGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAGCCACCCGGC
  901 ---------+---------+---------+---------+---------+---------+ 960
      GCGGTGGTAGGGCGTCCTGTGCCACTGGCTCTATTGCAGGAGGAGAGGGTCGGTGGGCCG

  b     A  T  I  P  Q  D  T  V  T  E  I  T  S  S  S  P  S  H  P  A  -

      CAACTCCTTCTACTACCCACGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGACACTGGT
  961 ---------+---------+---------+---------+---------+---------+ 1020
      GTTGAGGAAGATGATGGGTGCCGACTTCCGGGACGGAGGGTAGCGGTCCCACTGTGACCA

  b     N  S  F  Y  Y  P  R  L  K  A  L  P  P  I  A  R  V  T  L  V  -

      GCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGCAGGGA
 1021 ---------+---------+---------+---------+---------+---------+ 1080
      CGCCGACGCTGTCTCGGGGTCCCGGAAGTAGGGAGGGCGGGGTCAGGACGGGTCGTCCCT

  b     R  L  R  Q  S  P  R  A  F  I  P  P  A  P  V  L  P  S  R  D  -

      CAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTCCCT
 1081 ---------+---------+---------+---------+---------+---------+ 1140
      GTTACTCTAACATCTGTCGCGGAGTCAAGGTCTTTGCGGCGACCTGACGCTCCAGAGGGA

  b     N  E  I  V  D  S  A  S  V  P  E  T  P  L  D  C  E  V  S  L  -
```

FIGURE 4 - continued

```
      GTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGAC
1141  ---------+---------+---------+---------+---------+---------+  1200
      CACCAGCAGGACCCCTGACACGCCTCCGGTGACACCCTCCGAGCCCTGGTTCTCGTCCTG

b      W   S   S   W   G   L   C   G   G   H   C   G   R   L   G   T   K   S   R   T   -


      TCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGA
1201  ---------+---------+---------+---------+---------+---------+  1260
      AGCGATGCAGGCCCAGGTCGGGCGGTTGTTGCCCTCGGGGACGGGGCTCGAGCTTCTTCT

b      R   Y   V   R   V   Q   P   A   N   N   G   S   P   C   P   E   L   E   E   E   -


      GGCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGCAGCCCCTGGGGCCCC
1261  ---------+---------+---------+---------+---------+---------+  1320
      CCGACTCACGCAGGGACTATTGACGCAGATTCTGGTCTCGGGGCGTCGGGGACCCCGGGG

b      A   E   C   V   P   D   N   C   V   *                                    -


      CCGGAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCA
1321  ---------+---------+---------+---------+---------+---------+  1380
      GGCCTCGGTACCCCACAGCCCCCGAGGACACGTCCGAGTACGACGTCCGCCGGCTCCCGT


      CAGGGGGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAA
1381  ---------+---------+---------+---------+---------+---------+  1440
      GTCCCCCAAAGCGCGACGAGGACTGGCGCCACTCCGGCGCGGCTGGTAGAGACGTGACTT


      GGGCCCTCTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCT
1441  ---------+---------+---------+---------+---------+---------+  1500
      CCCGGGAGACCACCGGCCGTGCCCGTAACCCTTTGTCGGAGGAGGAAAGGGTTGGAACGA


      TCTTAGGGGCCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCAT
1501  ---------+---------+---------+---------+---------+---------+  1560
      AGAATCCCCGGGGGCACAGGGCAGACGAGAGTCGGAGGAGGAGGACGTCCTATTTCAGTA


      CCCCAAGGCTCCAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGA
1561  ---------+---------+---------+---------+---------+---------+  1620
      GGGGTTCCGAGGTCGATGAGATTTAATACAGAGGAATATTCAATAACGACGAGGTCCTCT


      TTGTCCTTCATCGTCCAGGGGCCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTG
1621  ---------+---------+---------+---------+---------+---------+  1680
      AACAGGAAGTAGCAGGTCCCCGGACCGAGGGTGCACCAACGTCTATGGAGTCTGGACCAC


      CTCTAGGCTGTGCTGAGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAA
1681  ---------+---------+---------+---------+---------+---------+  1740
      GAGATCCGACACGACTCGGGTGAGAGGGCTCCCGCGTAGGTTCGCCCCCGGTGAACTCTT


      GTGAATAAATGGGGCGGTTTCGGAAGCGTC
1741  ---------+---------+---------+  1770
      CACTTATTTACCCCGCCAAAGCCTTCGCAG
```
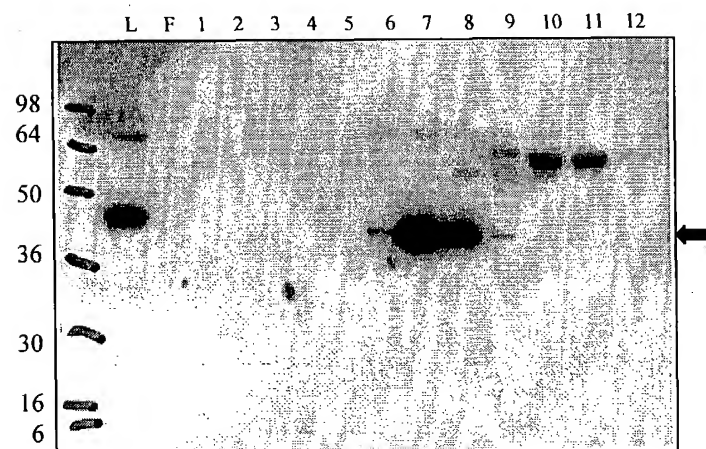
FIGURE 5

Expression of *Rg1* mRNA in human tissues
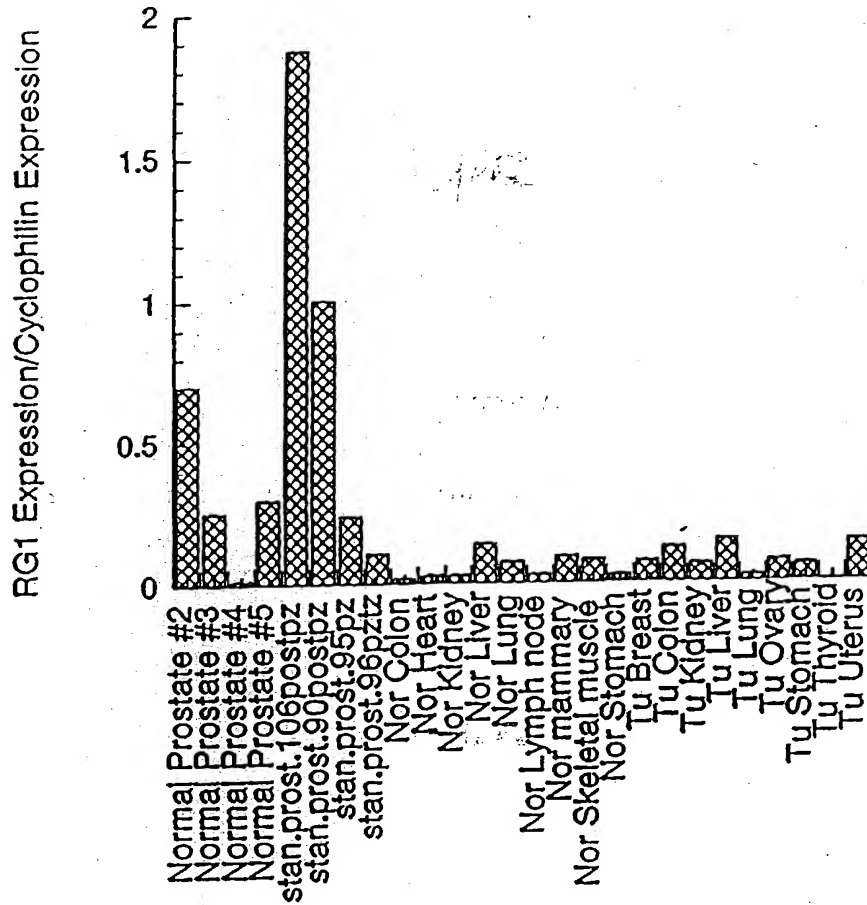
FIGURE 6

**Purification of Native RG1 Protein Secreted
by LNCaP Cells.**

FIGURE 7

hIgG$_1$ ProstaScint   A   B   C

% ID per gram

Time post injection (hrs)

● Blood   □ Tumor   ▲ Liver

FIGURE 8

Mean Tumor Volume (mm^3)

Day post single IP dose

- Saline
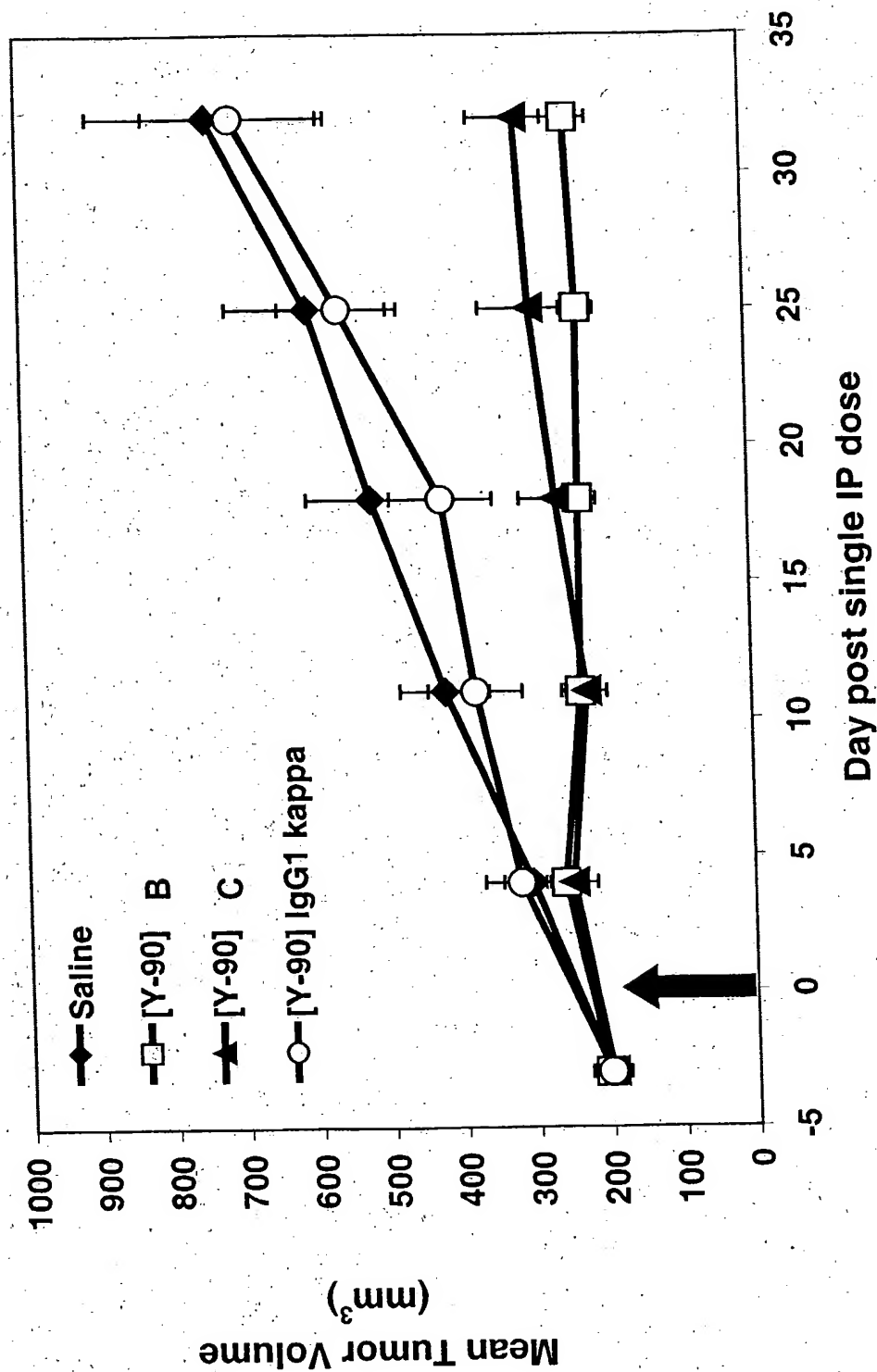- [Y-90] B
- [Y-90] C
- [Y-90] IgG1 kappa
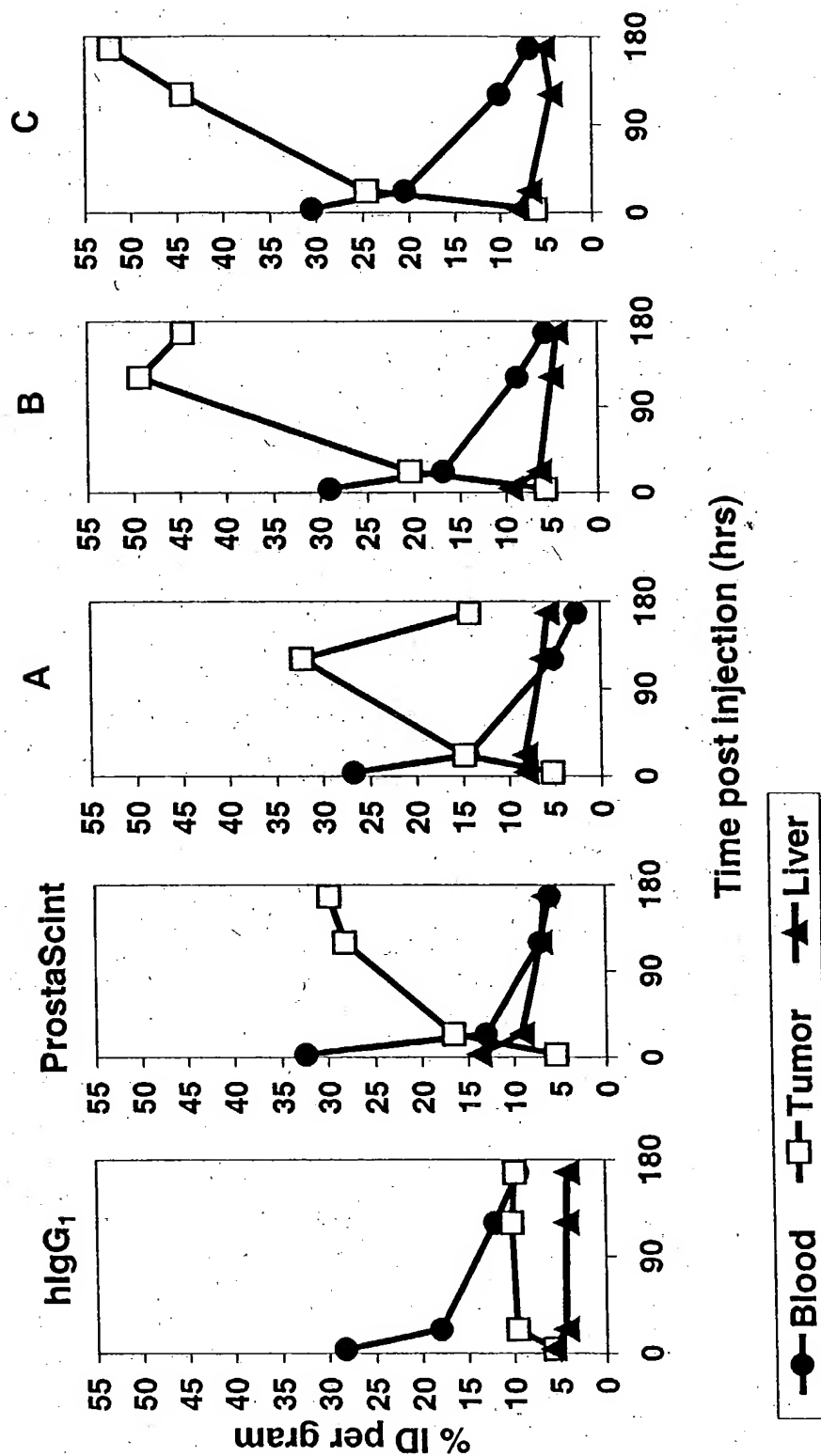
FIGURE 9

huMAb B Variable Region Sequences

V_L

```
  1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVS  50

 51 SSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE 100

101 PEDFAVYYCQQYSSSLTFGGGTKVEIK                        150
```

V_H

```
  1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVHPGGSLRLSCAGSGFTFSS  50

 51 YVMHWLRQAPGKGLEWVSVIGTGGVTHYADSVKGRFTISRDNAKNSLYLQ 100

101 MNSLRAEDMAMYYCARWGYYGSGSYENDAFDIWGQGTMVTVSSASTK    150
```

B_3M, V_H (mutations in bold)

```
  1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVQPGGSLRLSCAGSGFTFSS  50

 51 YVMHWLRQAPGKGLEWVSVIGTGGVTHYADSVKGRFTISRDNAKNSLYLQ 100

101 MNSLRAEDTAVYYCARWGYYGSGSYENDAFDIWGQGTMVTVSSASTK    150
```

CDR sequences (1,2,and 3) for each variable region are underlined

FIGURE 10

HuMAb C Variable Region Sequences

V_L

```
  1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVS  50

 51 SSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE 100

101 PEDFAVYYCQQYGSSLTFGGGTKVEIK                        150
```

V_H

```
  1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVHPGGSLRLSCAGSGFTFSS  50

 51 YVMHWVRQAPGKGLEWVSVIGTGGVTNYADSVKGRFTISRDNAKNSLYLQ 100

101 MNSLRAEDMAVYYCARWGDWDDAFDIWGQGTMVTVSSASTK          144
```

C_2m, V_H (mutations in bold)

```
  1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVQPGGSLRLSCAGSGFTFSS  50

 51 YVMHWVRQAPGKGLEWVSVIGTGGVTNYADSVKGRFTISRDNAKNSLYLQ 100

101 MNSLRAEDTAVYYCARWGDWDDAFDIWGQGTMVTVSSASTK          144
```

CDR sequences (CDR 1,2,and 3) for each variable region are underlined